

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 23:06:45 ; Search time 23.77 Seconds
(without alignments)
1423.712 Million cell updates/sec

Title: US-09-497-822a-19
Perfect score: 4912
Sequence: 1 MEVQLGLGRVYPRPFSKTYR.....SVQVQKILSGKVKPIVFHTQ 923

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	1	ANDR_HUMAN
2	4794	97.6	911	1	ANDR_PANTR
3	4694	95.6	895	1	ANDR_PAPHA
4	4678	95.2	895	1	ANDR_MACFA
5	4404.5	89.7	884	1	ANDR_EULFC
6	4319	87.9	907	1	ANDR_CANFA
7	4200.5	85.5	902	1	ANDR_MOUSE
8	4176	85.0	899	1	ANDR_MOUSE
9	3509.5	71.4	709	1	ANDR_RABIT
10	1262.5	25.7	930	1	PRGR_RABIT
11	1256	25.6	933	1	PRGR_HUMAN
12	1234	25.1	923	1	PRGR_RAT
13	1218	24.8	786	1	PRGR_CHICK
14	1205	24.5	923	1	PRGR_MOUSE
15	1116	22.7	377	1	PRGR_SHEEP
16	1092	22.2	981	1	MCR_RAT
17	1078.5	22.0	984	1	MCR_HUMAN
18	1069	21.8	795	1	GCR_RAT
19	1063.5	21.7	783	1	GCR_MOUSE
20	1053.5	21.4	776	1	GCR_XENLA
21	1053.5	21.4	777	1	GCR_SAGO
22	1046.5	21.3	777	1	GCR_AOTNA
23	1042	21.2	777	1	GCR_HUMAN
24	1042	21.2	778	1	GCR_SATSC
25	1041.5	21.2	777	1	GCR_SATBB
26	1034	21.1	612	1	MCR_XENLA
27	1033.5	21.0	776	1	GCR_TUGCB
28	1023	20.8	758	1	GCR_ONCMY
29	1014	20.6	977	1	MCR_TUGCB
30	1005	20.5	807	1	GCR_PAROL
31	996	20.3	771	1	GCR_CAVPO
32	970.5	19.8	703	1	GCR_PIG
33	509	10.4	180	1	PRGR_MACEU

34	502	10.2	595	1	ESR1_PIG	O29040 sus scrofa
35	498.5	10.1	594	1	ESR1_HORSE	O3tv98 equus caball
36	491	10.0	586	1	ESR1_XENLA	P81559 xenopus lae
37	485.5	9.9	600	1	ESR1_RAT	P06211 rattus norv
38	481	9.8	595	1	ESR1_HUMAN	P03372 homo sapien
39	474.5	9.7	595	1	ESR1_MESAU	O9qz35 mesocricetu
40	474	9.6	589	1	ESR1_CHICK	P06212 gallus gall
41	474	9.6	599	1	ESR1_MOUSE	P19785 mus musculu
42	470.5	9.6	569	1	ESR1_BRARE	P57717 brachydanio
43	469.5	9.6	622	1	ESR1_ONCMY	P16058 oncorhynch
44	465	9.5	587	1	ESR1_POEGU	P51250 poephila gu
45	461.5	9.4	620	1	ESR1_ORYZA	P50241 oryzias lat

ALIGNMENTS

RESULT 1	
ID ANDR_HUMAN	
AC P10275;	STANDARD; PRT; 919 AA.
DT 01-MAR-1989 (Rel. 10, Created)	
DT 01-APR-1990 (Rel. 14, Last sequence update)	
DT 20-AUG-2001 (Rel. 40, Last annotation update)	
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).	
GN AR OR NR3C4 OR DHTR.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=89112208; PubMed=3216866;	
RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,	
RA French F.S., Wilson E.M.;	
RT "The human androgen receptor: complementary deoxyribonucleic acid	
RL cloning, sequence analysis and gene expression in prostate.";	
RN [2]	
RP SEQUENCE FROM N.A., AND VARIANT CAIS MET-866.	
RX MEDLINE=90083302; PubMed=2594783;	
RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,	
RA Wilson E.M., French F.S.;	
RT "Sequence of the intron/exon junctions of the coding region of the	
RT human androgen receptor gene and identification of a point mutation	
RL in a family with complete androgen insensitivity";	
RN [3]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=90258935; PubMed=2342476;	
RA Govindan M.V.;	
RT "Specific region in hormone binding domain is essential for hormone	
RL binding and trans-activation by human androgen receptor.";	
RN [4]	
RP SEQUENCE FROM N.A.	
RX TISSUE=Prostate;	
RA MEDLINE=89017168; PubMed=3174628;	
RA Chang C., Kokontis J., Liao S.;	
RT "Structural analysis of complementary DNA and amino acid sequences of	
RL human and rat androgen receptors.";	
RN [5]	
RP SEQUENCE FROM N.A.	
RX TISSUE=Prostate;	
RA MEDLINE=89098909; PubMed=2911578;	
RA Tilley W.D., Marcelli M., Wilson J.D., McPhaul M.J.;	
RT "Characterization and expression of a cDNA encoding the human androgen	
RL receptor.";	
RN [6]	
RP SEQUENCE FROM N.A.	
RX TISSUE=Prostate;	

RX MEDLINE=91155943; PubMed=22933020;
 RA Marcelli M., Tilley W.D., Wilson C.M., Griffin J.E., Wilson J.D.,
 RA McPhaul M.J.;
 RT "Definition of the human androgen receptor gene structure permits the
 RT identification of mutations that cause androgen resistance: premature
 RT termination of the receptor protein at amino acid residue 588 causes
 RT complete androgen resistance";
 RL Mol. Endocrinol. 4:1105-1116(1990). X
 RN [7]
 RN SEQUENCE OF 189-919 FROM N.A.
 RN MEDLINE=88178111; PubMed=3353726;
 RX Chang C., Kokontis J., Liao S.;
 RA "Molecular cloning of human and rat complementary DNA encoding
 RT androgen receptors";
 RL Science 240:324-326(1988). ?
 RN [8]
 RN SEQUENCE OF 468-919 FROM N.A.
 RN MEDLINE=88240407; PubMed=3377788;
 RX Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M.,
 RA Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M.,
 RA Mulder E., Brinkmann A.O.;
 RT "Cloning, structure and expression of a cDNA encoding the human
 RT androgen receptor";
 RL Biochem. Biophys. Res. Commun. 153:241-246(1988). ?
 RN [9]
 RN POLYMORPHISM OF POLY-GLN REGION.
 RX MEDLINE=92220629; PubMed=1561105;
 RA Sleddens H.F.B.M., Oostra B.A., Brinkmann A.O., Trapman J.;
 RT "Trinucleotide repeat polymorphism in the androgen receptor gene
 RT (AR)";
 RL Nucleic Acids Res. 20:1427-1428(1992). X
 RN [10]
 RN POLYMORPHISM OF POLY-GLY REGION.
 RX Lu J., Danielson M.;
 RT TISSUE-Blood;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RN POLYMORPHISM OF POLY-GLN REGION.
 RX MEDLINE=97250535; PubMed=9096391;
 RA Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Brufsky A.,
 RA Talcott J., Hennekens C.H., Kantoff P.W.;
 RT "The CAG repeat within the androgen receptor gene and its
 RT relationship to prostate cancer";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3320-3323(1997). X
 RN [12]
 RN ERRATUM.
 RA Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Dahl D.,
 RA Brufsky A., Talcott J., Hennekens C.H., Kantoff P.W.;
 RL Proc. Natl. Acad. Sci. U.S.A. 94:8272-8272(1997).
 RN [13]
 RN REVIEW ON VARIANTS.
 RX MEDLINE=93092459; PubMed=1458719;
 RA Pinsky L., Trifiro M.A., Kaufman M., Beitel L.K., Mhatre A.,
 RA Kazemi-Esfarjani P., Sabbaghian N., Lumbroso R., Alvarado C.,
 RA Vasiliou M., Gottlieb B.;
 RT "Androgen resistance due to mutation of the androgen receptor";
 RL Clin. Invest. Med. 15:456-462(1992). X
 RN [14]
 RN REVIEW ON VARIANTS AIS.
 RX MEDLINE=93339360; PubMed=8339746;
 RA Brown T.R., Scherer P.A., Chang Y.-T., Migeon C.J., Ghirri P.,
 RA Muroto K., Zhou Z.;
 RT "Molecular genetics of human androgen insensitivity";
 RL Eur. J. Pediatr. 152 Suppl. 2:S62-S69(1993). X
 RN [15]
 RN REVIEW ON VARIANTS.
 RX MEDLINE=94059770; PubMed=8240973;
 RA Sultan C., Lumbroso S., Poujol N., Belon C., Boudon C.,
 RA Lobaccaro J.-M.;
 RT "Mutations of androgen receptor gene in androgen insensitivity
 RT syndromes";
 RL J. Steroid Biochem. Mol. Biol. 46:519-530(1993). X
 RN [16]
 RN REVIEW ON VARIANTS.
 RX MEDLINE=95023089; PubMed=7937057;
 RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.;
 RT "The androgen receptor gene mutations database";
 RL Nucleic Acids Res. 22:3560-3562(1994). X
 RN [17]
 RN REVIEW ON VARIANTS.
 RX MEDLINE=95352489; PubMed=7626493;
 RA Brinkmann A.O., Jenster G., Ris-Stalpers C., van der Korput J.A.G.M.,
 RA Bruggenwirth H.T., Boehmer A.L.M., Trapman J.;
 RT "Androgen receptor mutations";
 RL J. Steroid Biochem. Mol. Biol. 53:443-448(1995). X
 RN [18]
 RN REVIEW ON VARIANTS.
 RX MEDLINE=97169385; PubMed=9016528;
 RA Gottlieb B., Trifiro M.A., Lumbroso R., Vasiliou D.M., Pinsky L.;
 RT "The androgen receptor gene mutations database";
 RL Nucleic Acids Res. 25:158-162(1997). X
 RN [19]
 RN VARIANT LNCAP ALA-877.
 RX MEDLINE=91083633; PubMed=2260966;
 RA Veldscholte J., Ris-Stalpers C., Kuiper G.G.J.M., Jenster G.,
 RA Berrevoets C.A., Claassen E., van Rooij H.C.J., Trapman J.,
 RA Brinkmann A.O., Mulder E.;
 RT "A mutation in the ligand binding domain of the androgen receptor of
 RT human LNCap cells affects steroid binding characteristics and
 RT response to anti-androgens";
 RL Biochem. Biophys. Res. Commun. 173:534-540(1990). X
 RN [20]
 RN VARIANTS CAIS CYS-774; GLN-831 AND MET-866.
 RX MEDLINE=91186983; PubMed=2082179;
 RA Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J.,
 RA Corfen J.L.;
 RT "Functional characterization of naturally occurring mutant androgen
 RT receptors from subjects with complete androgen insensitivity";
 RL Mol. Endocrinol. 4:1759-1772(1990). X
 RN [21]
 RN VARIANT CYS-774.
 RX MEDLINE=91310758; PubMed=1856263;
 RA Marcelli M., Tilley W.D., Zoppi S., Griffin J.E., Wilson J.D.,
 RA McPhaul M.J.;
 RT "Androgen resistance associated with a mutation of the androgen
 RT receptor at amino acid 772 (Arg->Cys) results from a combination of
 RT decreased messenger ribonucleic acid levels and impairment of
 RT receptor function";
 RL J. Clin. Endocrinol. Metab. 73:318-325(1991). X
 RN [22]
 RN VARIANT CAIS PRO-617.
 RX MEDLINE=91154385; PubMed=1999491;
 RA Marcelli M., Zoppi S., Grino P.B., Griffin J.E., Wilson J.D.,
 RA McPhaul M.J.;
 RT "A mutation in the DNA-binding domain of the androgen receptor gene
 RT causes complete testicular feminization in a patient with
 RT receptor-positive androgen resistance";
 RL J. Clin. Invest. 87:1123-1126(1991). X
 RN [23]
 RN VARIANT PAIS CYS-763.
 RX MEDLINE=91185626; PubMed=2010552;
 RA McPhaul M.J., Marcelli M., Tilley W.D., Griffin J.E.,
 RA Isidro-Gutierrez R.F., Wilson J.D.;
 RT "Molecular basis of androgen resistance in a family with a qualitative
 RT abnormality of the androgen receptor and responsive to high-dose
 RT androgen therapy";
 RL J. Clin. Invest. 87:1413-1418(1991). X
 RN [24]
 RN VARIANTS CAIS ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A.
 RX MEDLINE=92131007; PubMed=1775137;
 RA Ris-Stalpers C., Trifiro M.A., Kuiper G.G.J.M., Jenster G., Romalo G.,
 RA Sai T., van Rooij H.C.J., Kaufman M., Rosenfield R.L., Liao S.,
 RA Schweikert H.-U., Trapman J., Pinsky L., Brinkmann A.O.;
 RT "Substitution of aspartic acid-686 by histidine or asparagine in the
 RT human androgen receptor leads to a functionally inactive protein with
 RT altered hormone-binding characteristics";

[illegible]

O97775;
 30-MAY-2000 (Rel. 39, Created)
 30-MAY-2000 (Rel. 39, Last sequence update)
 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
 GN OR NR3C4.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OX NCBI_Taxid=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98404153; PubMed=9732460;
 RA Choong C.S., Kempainen J.A., Wilson E.M.;
 RT "Evolution of the primate androgen receptor: a structural basis for
 RT disease.";
 RL J. Mol. Evol. 47:334-342(1998).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL, STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR3 SUBFAMILY.
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[illegible]

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[1]
SEQUENCE FROM N.A.
MEDLINE=98404153; PubMed=9732460;
Choong C.S., Kempainen J.A., Wilson E.M.;
"Evolution of the primate androgen receptor: a structural basis for
disease.";
J. Mol. Evol. 47:334-344(1998)
-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NR3 SUBFAMILY.
-----
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EMBL; U94176; AAC73047.1; --
HSSP; P06536; IRGB.
InterPro; IPR001103; Androgen_recep.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; zf-C4.
Pfam; PF02166; Androgen_recep; 1.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00521; ANDROGENR.
SMART; SM00430; HOL1; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
zinc-finger; Steroid-binding.
KW DOMAIN 1 533 MODULATING (BY SIMILARITY).
FT NUCLEAR RECEPTOR-TYPE.
FT N_FING 535 600
FT ZN_FING 535 555
FT ZN_FING 571 595
FT C4-TYPE.
FT DOMAIN 666 895 LIGAND-BINDING.
FT POLY-GLN.
FT POLY-GLN.
FT POLY-GLN.
FT POLY-GLN.
FT POLY-PRO.
FT POLY-ALA.
FT POLY-GLY.
FT DOMAIN 434 448
FT SEQUENCE 895 AA; 96478 MW; 9020C0DC67FILESD CRC64;

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Query Match 95.6%; Score 4694; DB 1; Length 895;
Best Local Similarity 96.1%; Pred. No. 4.5e-215;
Matches 887; Conservative 3; Mismatches 5; Indels 28; Gaps 2;

1 MEVQLGLGRVYPRPSKTYRGAFQNLFQSVREVIONQPRHPEAASAAPPGASLLLOQQ 60 QY
1 MEVQLGLGRVYPRPSKTYRGAFQNLFQSVREVIONQPRHPEAASAAPPGASL----- 54 Db
61 QQQQQQQQQQQQQQQQQQQQQQQETSPQQQQQQGGEGDSQAIHRRGPTGYLVLDEEQPSQ 120 QY
55 -----QQQQQQQQQQETSPQQQQQQGGEGDSQAIHRRGPTGYLVLDEEQPSQ 101 Db
121 POSALECHPERGCVPEPAAVAASKGLPQOLPAPPPEDDSSAAPSTLSLGLGPTFPGLSSCS 180 QY
102 POSALECHPERGCVPEPAAVAASKGLPQOLPAPPPEDDSSAAPSTLSLGLGPTFPGLSSCS 161 Db
181 ADLKDILSEASTMQLQQQQQEAIVSESSGGRARASGAPTSKDNVLTGTTSIDNAKE 240 QY
162 ADLKDILSEASTMQLQQQQQEAIVSESSGGRARASGAPTSKDNVLTGTTSIDNAKE 221 Db

RESULT	3	RESULT
ANDR_PAPHA	ANDR_PAPHA	STANDARD; PRT; 895 AA.
ID	ANDR_PAPHA	
AC	O97960;	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).	
GN	AR OR NR3C4.	
OS	Papio hamadryas (Hamadryas baboon).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;	
OC	Cercopithecoidea; Papio.	
OX	NCBI TaxID=9557;	
OX		

QY 241 LKAVSVSMGLGVLEALHSLSPGQRLGDCMYAPLLGVPAVRPTPCAPLAECCKSLDSDS 300
 Db 222 LKAVSVSMGLGVLEALHSLSPGQRLGDCMYAPLLGVPAVRPTPCAPLAECCKSLDSDS 281
 QY 301 AGKSTEDTAESPFGKYTKGLESGSAAAGSSGTLELPSTLSLYKSGALDEAAA 360
 Db 282 AGKSTEDTAESPFGKYTKGLESGSAAAGSSGTLELPSTLSLYKSGALDEAAA 341
 QY 361 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAQCRYGDLASLHGAG 420
 Db 342 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAQCRYGDLASLHGAG 401
 QY 421 AAGPGSGSPSAASSWHILFTAEQOLYXPCGGGGGGGGGGGGGGGGGGGGGGG 480
 Db 402 AAGPGSGSPSAASSWHILFTAEQOLYXPCGGGGGGGGGGGGGGGGGGGGGGG 462
 QY 481 VAPYGYTRPPQGLAGQSEDTAPDVYVPGMVSRVPYPSPTCVKSEMGPMWDSYSGPYGD 540
 Db 453 VAPYGYTRPPQGLAGQSEDTAPDVYVPGMVSRVPYPSPTCVKSEMGPMWDSYSGPYGD 512
 QY 541 MRLETARDHVLPIDYFPQKTCCLICGDEASGCHYGALTCGSKCVFFKRAAEGKQYLCA 600
 Db 513 MRLETARDHVLPIDYFPQKTCCLICGDEASGCHYGALTCGSKCVFFKRAAEGKQYLCA 572
 QY 601 SRNDCTIDKFRKNCPSCLRCYKCYEAGMTLGARKLKLGNLKLQEGEASSTTSPTET 660
 Db 573 SRNDCTIDKFRKNCPSCLRCYKCYEAGMTLGARKLKLGNLKLQEGEASSTTSPTET 632
 QY 661 OKLTVSHIGYECQPIFLNVLEAIEPVGVCAGHDNNPDPSFAALLSSNELGEROLVHV 720
 Db 633 OKLTVSHIGYECQPIFLNVLEAIEPVGVCAGHDNNPDPSFAALLSSNELGEROLVHV 692
 QY 721 KWAKALPGFRLHVDOMAVIOYQSWGLMVFMANGWRSETNVNSRMLYFAPDLVFNERYMH 780
 Db 693 KWAKALPGFRLHVDOMAVIOYQSWGLMVFMANGWRSETNVNSRMLYFAPDLVFNERYMH 752
 QY 781 KSRMYSQCVRMRLHLSQEGWLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYIK 840
 Db 753 KSRMYSQCVRMRLHLSQEGWLQITPOEFLCMKALLFSIIPVDGLKNOKFFDELRMNYIK 812
 QY 841 ELDRIIAKRKNTSCSRFRFVOLTLLKLDVQPIARELHQFTFDLLIKSHMYSVDPFEMMA 900
 Db 813 ELDRIIAKRKNTSCSRFRFVOLTLLKLDVQPIARELHQFTFDLLIKSHMYSVDPFEMMA 872
 QY 901 ELISVQPKILSGKVKPIYFHTQ 923
 Db 873 ELISVQPKILSGKVKPIYFHTQ 895

RESULT 4
 ID ANDR MACFA
 AC 097952; STANDARD; PRT; 895 AA.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
 GN AR OR NR3C4.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96404153; PubMed=9732460;
 RA Choong C.S., Kempainen J.A., Wilson E.M.;
 RT "Evolution of the primate androgen receptor: a structural basis for
 disease".
 RL J. Mol. Evol. 47:334-342 (1998).
 CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUROPEATIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR3 SUBFAMILY.
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 CC EMBL; U94179; AAC73050.1; -;
 CC HSP; P06536; IRGD
 CC InterPro; IPR001103; Androgen_recep.
 CC InterPro; IPR000536; Hormone_rec_lig.
 CC InterPro; IPR001628; zf-C4.
 CC Pfam; PF02166; Androgen_recep; 1.
 CC Pfam; PF00104; hormone_rec; 1.
 CC Pfam; PF00105; zf-C4; 1.
 CC PRINTS; PR00047; STROLDIFINGER.
 CC PRINTS; PR00521; ANDROGENR.
 CC SMART; SM00430; HOLI; 1.
 CC SMART; SM00399; ZnF_C4; 1.
 CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Steroid-binding.
 KW DOMAIN 1 533 MODULATING (BY SIMILARITY).
 FT ZN_BIND 535 600 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 535 555 C4-TYPE.
 FT ZN_FING 571 595 C4-TYPE.
 FT DOMAIN 666 895 LIGAND-BINDING.
 FT DOMAIN 55 62 POLY-GLN.
 FT DOMAIN 68 74 POLY-GLN.
 FT DOMAIN 178 182 POLY-GLN.
 FT DOMAIN 357 366 POLY-PRO.
 FT DOMAIN 381 387 POLY-ALA.
 FT DOMAIN 434 448 POLY-GLY.
 SQ SEQUENCE 895 AA; 96494 MW; A3EB17916F43A097 CRC64;
 Query Match 95.2%; Score 4678; DB 1; Length 895;
 Best Local Similarity 95.9%; Pred. No. 2.6e-214;
 Matches 886; Conservative 2; Mismatches 6; Indels 30; Gaps 3;
 QY 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNPGRHPEAASAPPGASLLILOOQ 60
 Db 1 MEVOLGLGRVYPRPPSKTYRGAFQNLFSQSVREVIQNPGRHPEAASAPPGASL----- 54
 QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
 Db 55 -----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 100
 QY 120 QPOSALCHPERGCVPEPGAASAKGLPQLPAPDEDDSAAPSTLSLGLTFFGLSSC 179
 Db 101 QPOSALCHPERGCVPEPGAASAKGLPQLPAPDEDDSAAPSTLSLGLTFFGLSSC 160
 QY 180 SADLKILSEASTMQLQQQQQEAIVSESSSSGRAREASGAPTSSKDNLYLGGTSTISDNK 239
 Db 161 STDLDKILSEASTMQLQQQQQEAIVSESSSSGRAREASGAPTSSKDNLYLGGTSTISDNK 220
 QY 240 ELCKAVSVSMGLGVLEALHSLSPGQRLGDCMYAPLLGVPAVRPTPCAPLAECCKSLDD 299
 Db 221 ELCKAVSVSMGLGVLEALHSLSPGQRLGDCMYAPLLGVPAVRPTPCAPLAECCKSLDD 280
 QY 300 SAGKSTEDTAESPFGKYTKGLESGSAAAGSSGTLELPSTLSLYKSGALDEAAA 359
 Db 281 SAGKSTEDTAESPFGKYTKGLESGSAAAGSSGTLELPSTLSLYKSGALDEAAA 340
 QY 360 YQSRDYNNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAQCRYGDLASLHGAG 419

[illegible]

QY 540 DMRLETARDHVLPIIDYFPQKTCICGDEASGCHYGALTCGCKVFFKRAAEGKOKYLC 599
 Db 501 DVRLTARDHVLPIIDYFPQKTCICGDEASGCHYGALTCGCKVFFKRAAEGKOKYLC 560
 QY 600 ASRNDCTIDFRKRNKPCSRKRCYKCYEAGMTLGARKLKGLNKLQEGEGASSTTSPTTEET 659
 Db 561 ASRNDCTIDFRKRNKPCSRKRCYKCYEAGMTLGARKLKGLNKLQEGEGASSTTSPTTEES 620
 QY 660 TOKLTVSHIEGYECOPILFNLVLEAIEPBGVVCAGHNNQDPSFAALLSSNLEIGEROLVHV 719
 Db 621 SOKLTVSHIEGYECOPILFNLVLEAIEPBGVVCAGHNNQDPSFAALLSSNLEIGEROLVHV 680
 QY 720 VKWAKALPGFRNLHVDQMAVIOYSNMGLMVFAMGWRSTFNNSRMLYFAPDLVFNERYM 779
 Db 681 VKWAKALPGFRNLHVDQMAVIOYSNMGLMVFAMGWRSTFNNSRMLYFAPDLVFNERYM 740
 QY 780 HKSRMYSQCVRMHRLHSDQFGLWLOITPQEFCLMKALLFSIIPVDGLKNQKFFDELRMNYI 839
 Db 741 HKSRMYSQCVRMHRLHSDQFGLWLOITPQEFCLMKALLFSIIPVDGLKNQKFFDELRMNYI 800
 QY 840 KELDRIACKRNKPTSCSRFFYOLTLLDVSQPIARELHOFTFDLLIKSHMYSVDPEMM 899
 Db 801 KELDRIACKRNKPTSCSRFFYOLTLLDVSQPIARELHOFTFDLLIKSHMYSVDPEMM 860
 QY 900 AEIISVQVKILSGKVKPIYFHTQ 923
 Db 861 AEIISVQVKILSGKVKPIYFHTQ 884

RESULT 6
 ANDR_CANFA STANDARD; PRT; 907 AA.
 ID ANDR_CANFA Q9TT90;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
 GN AR OR NR3C4.
 OS Canis familiaris (Dog)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu B., Smock S.L., Castleberry T.A., Owen T.A.;
 RT "Molecular cloning and functional characterization of the canine
 androgen receptor."
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: ANDROGEN RECEPTOR. THE RECEPTORS ARE INVOLVED IN
 CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
 CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR3 SUBFAMILY.
 CC
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 CC
 CC EMBL; AF197950; AAF18084.1;
 CC InterPro; IPR001103; Androgen_recep.
 CC InterPro; IPR000536; Hormone_rec_lig.
 CC InterPro; IPR001628; zf-C4.
 CC Pfam; PF02166; Androgen_recep; 1.
 CC Pfam; PF00104; hormone_rec; 1.
 CC Pfam; PF00105; zf-C4; 1.

DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; znF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 FT zinc-finger; Steroid-binding.
 FT DOMAIN 1 545 MODULATING (BY SIMILARITY).
 FT DNA_BIND 547 612 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 547 567 C4-TYPE.
 FT ZN_FING 583 607 C4-TYPE.
 FT DOMAIN 678 907 LIGAND-BINDING.
 FT DOMAIN 55 64 POLY-GLN.
 FT DOMAIN 70 76 POLY-GLN.
 FT DOMAIN 131 134 POLY-GLN.
 FT DOMAIN 180 202 POLY-GLN.
 FT DOMAIN 329 332 POLY-SER.
 FT DOMAIN 375 384 POLY-PRO.
 FT DOMAIN 399 405 POLY-ALA.
 SQ SEQUENCE 907 AA; 98726 MW; C6619F78DD2338AF CRC64;

Query Match 87.9%; Score 4319; DB 1; Length 907;
 Best Local Similarity 87.3%; Pred. No. 2.3e-197;
 Matches 822; Conservative 20; Mismatches 46; Indels 54; Gaps 5;

QY 1 MEVOLGLGRVYPRPSKTYRCAFONLFSQSVREVTONCPRHPEAASAPPGASLLLLQQQ 60
 Db 1 MEVOLGLGRVYPRPSKTYRCAFONLFSQSVREVTONCPRHPEAASAPPGASLLLLQQQ 60
 QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
 Db 55 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 102
 QY 120 QPSALECHPERGCVPEFGAANAASKGLPOLPAPPDEDDSAAPSTLSLLGTFPGLSSC 179
 Db 103 QRSASRGHPESACVPEPGVTSATGKGLQQQAPPDENDDSAAPSTLSLLGTFPGLSSC 162
 QY 180 SADLKDLISEASTMQLL-----QQQQQEAQSESSSSSGRAEASGAPT 221
 Db 163 STDLDKDLISEAGTMQLLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 222
 QY 222 SKDNYLGGTSTISDNAKELCAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAV 281
 Db 223 SKDSYLGGSSTISDSAKELCAVSVSMGLGVEALEHLSPEQLRGDCMYAPLLGVPPAV 282
 QY 282 RPTPCAPLAECKGLDSDSAGKSTEDTAETSPKGGYTKGLESGLCGSSAAGSGTL 341
 Db 283 R-PCAPLAECKGLDSDSAGKSTEDTAETSPKGGYTKGLESGLCGSSAAGSGTL 340
 QY 342 ELFTSLYKSGALDEAAAYQSRDYNFPLALAGPPPPPPPPHARIKLENPLDYGSAAW 401
 Db 341 EMPSTLSLYKSGALDEAAAYQSRDYNFPLSLGPPPPPPHARIKLENPLDYGSAAW 400
 QY 402 AAAAQCRCYGLASLHGAGAGCGSGSPSAASSSSWHTLFTAEGLYPCGGGGGGGGG 461
 Db 401 AAAAQCRCYGLASLHGAGAGCGSGSPSAASSSSWHTLFTAEGLYPCGGGGGGGGG 460
 QY 462 GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 521
 Db 461 DG-----GSVAPGYTRPQGLAGQEDFTAPDVWYPPGGMWVRVPSPT 505
 QY 522 CVKSEMGPMWDSYSGPYGDMRLTARDHVLPIIDYFPQKTCICGDEASGCHYGALTCG 581
 Db 506 CVKSEMGPMWDSYSGPYGDMRLTARDHVLPIIDYFPQKTCICGDEASGCHYGALTCG 565
 QY 582 SKVFFKRAEGRKQYLCASRNDCCTDKFRKNCPSCLRKCVEAGMTLGARKLKGLNL 641
 Db 566 SKVFFKRAEGRKQYLCASRNDCCTDKFRKNCPSCLRKCVEAGMTLGARKLKGLNL 625
 QY 642 KLOEGEGASSTTSPTETTKLTVSHIEGYECOPILFNLVLEAIEPBGVVCAGHNNQDPSF 701
 Db 626 KLOEGEGASSTTSPTETTKLTVSHIEGYECOPILFNLVLEAIEPBGVVCAGHNNQDPSF 685
 QY 702 AALLSSNLGELGRQLVHVVKWAKALFGFRNLHVDQMAVIOYSNMGLMVFAMGWRSTFN 761


```

Db 397 AAAACRYGLASLHSGSVAGPTGSPATASSWHTLTAEGLQYGP----- 445
QY 463 GGGGGGGGGGGGAGAVAPYGYTRPPGCLAGQESDFTAPDWWYEGMVSRVPVSPPTC 522
Db 446 ----GGGGSSSPDAGPAPYGYTRPPGCLAGQESDFTAPDWWYEGMVSRVPVSPSC 501
QY 523 VKSEMGWMDYSYSGPYGDMRLTARDHVLPIDYFPPQKTCCLICGDEASGCHYALTCGS 582
Db 502 VKSEMGWMDYSYSGPYGDMRLTARDHVLPIDYFPPQKTCCLICGDEASGCHYALTCGS 561
QY 583 CKVFFKRAAEKGKYLKASRNDCTIDKFRKNCPCSLRKCCEAGMTLGARKLKGLNKL 642
Db 562 CKVFFKRAAEKGKYLKASRNDCTIDKFRKNCPCSLRKCCEAGMTLGARKLKGLNKL 621
QY 643 LOEGEASSTSTTEETOKLVSHTEGECQPIFNVLNLEAEPGVVCAAGHNNQPDSPA 702
Db 622 LOEGEASSTSTTEETOKLVSHTEGECQPIFNVLNLEAEPGVVCAAGHNNQPDSPA 681
QY 703 ALLSSLNGLGERQLVHVWAKALPGFRNLHVDDQAVIOYSMGLMVFAMGWRSTNNV 762
Db 682 ALLSSLNGLGERQLVHVWAKALPGFRNLHVDDQAVIOYSMGLMVFAMGWRSTNNV 741
QY 763 SRMLYFAPDLVFNEMRHKSRMYSCVVRHLSQEFGLQITPQEFCLMKALLFSIIPV 822
Db 742 SRMLYFAPDLVFNEMRHKSRMYSCVVRHLSQEFGLQITPQEFCLMKALLFSIIPV 801
QY 823 DGLKNOKFDELKRNMYKELDRILIAKRNKPTSCSRFFVQLTKLDSVOPIARELHQFTF 882
Db 802 DGLKNOKFDELKRNMYKELDRILIAKRNKPTSCSRFFVQLTKLDSVOPIARELHQFTF 861
QY 883 DLLIKSHMVSDVPEPMAETIISVQVKILSGKVPYFHTQ 923
Db 862 DLLIKSHMVSDVPEPMAETIISVQVKILSGKVPYFHTQ 902

RESULT 8
ID ANDR_MOUSE STANDARD: PRT; 899 AA.
AC P19091;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANDROGEN RECEPTOR (Q1HYDROTESTOSTERONE RECEPTOR).
GN AR OR NR3C4.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=90386642; PubMed=2403358;
RA He W.W., Fischer L.M., Sun S., Bilhartz D.L., Zhu X., Young C.Y.F.,
RA Kelley D.B., Tindall D.J.;
RT "Molecular cloning of androgen receptors from divergent species with
RT a polymerase chain reaction technique: complete cDNA sequence of the
RT mouse androgen receptor and isolation of androgen receptor cDNA
RT probes from dog, guinea pig and clawed frog."
RL Biochem. Biophys. Res. Commun. 171:697-704(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91133433; PubMed=2178222;
RA Gaspar M.L., Neo T., Tosi M.;
RT "Structure and size distribution of the androgen receptor mRNA in
RT wild-type and Tfm/Y mutant mice."
RL Mol. Endocrinol. 4:1600-1610(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91354214; PubMed=1883336;
RA Faber P.W., King A., van Rooij H.C.J., Brinkmann A.O., de Both N.J.,
RA Trapman J.;
RT "The mouse androgen receptor. Functional analysis of the protein and

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RT RT
RL RL
RN RN
RP RP
RX RX
RA RA
RA French F.S.;
RT "A frameshift mutation destabilizes androgen receptor messenger RNA
RT in the Tfm mouse."
RL Mol. Endocrinol. 5:573-591(1991).
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS
CC ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;
CC HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE
CC HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA
CC SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; S56585; AAB19916.1; -
CC EMBL; X53779; CAA37795.1; -
CC EMBL; M37890; AAA37234.1; -
CC EMBL; X59592; CAA42160.1; -
CC PIR; A35895; A35895;
CC PIR; A37255; A37255;
CC PIR; A37908; A37908;
CC PIR; S17198; S17198;
CC PIR; S34398; S34398;
CC HSSP; P06536; 1RGD.
CC TRANSFAC; T00041; -
CC MGD; MGI:88064; Ar.
CC InterPro; IPR001103; Androgen_recep.
CC InterPro; IPR000536; Hormone_rec_llg.
CC InterPro; IPR001628; zf-C4.
CC Pfam; PF02166; Androgen_recep; 1.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00047; STROIDFINGER.
CC PRINTS; PR00521; ANDROGENR.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding.
CC DOMAIN 1 537 MODULATING (BY SIMILARITY).
CC DNA_BIND 539 604 NUCLEAR RECEPTOR-TYPE.
CC ZN_FING 539 559 C4-TYPE.
CC ZN_FING 575 599 C4-TYPE.
CC DOMAIN 670 899 LIGAND-BINDING.
CC DOMAIN 63 67 POLY-ARG.
CC DOMAIN 174 193 POLY-GLN.
CC DOMAIN 367 373 POLY-PRO.
CC DOMAIN 391 397 POLY-ALA.
CC DOMAIN 441 447 POLY-GLY.
CC SEQUENCE 899 AA; 98193 MW; FD9E07C07F7A568 CRC64;

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Query Match 85.0%; Score 4176; DB 1; Length 899;
 Best Local Similarity 84.1%; Pred. No. 1.3e-190;
 Matches 790; Conservative 40; Mismatches 53; Indels 56; Gaps 5;

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QY 1 MEVGLGRLVYPRPSKTYGAFQNLFSQSVREVIQNGPRHPPEASAAAPPASLLLLQQQ 60
Db 1 MEVGLGRLVYPRPSKTYGAFQNLFSQSVREVIQNGPRHPPEANAPPGACL----- 54
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
Db 55 -----QQQQTSPRRRRQQHTEDGSPQAHIRGTGYLALEEEQQPS 96
QY 120 QPSALECHPERGCVPPGAAVASKGLPOOLPAPDEDDSAAPSTLSLLGTPFPGLSSC 179
Db 97 QQAASCHPESSCLPPEGAATAPGKLPQPPAPPDQDDSAAPSTLSLLGTPFPGLSSC 156
QY 180 SADLKDLTSLASNTMOLLQ-----QQQQAASCHPESSCLPPEGAATAPGKLP 224
Db 157 SADLKDLTSLASNTMOLLQ-----QQQQAASCHPESSCLPPEGAATAPGKLP 215
QY 225 DNYLGSTSTSDNAKELCKAVSMGLGVLEHLSPGEOLRDCMYAPLLGVPPAVRPT 284
Db 216 DSYLGGNSTISDSAKELCKAVSMGLGVLEHLSPGEOLRDCMYAPLLGVPPAVRPT 275
QY 285 PCAPLAECKSLDDDSAGKSTEDTAESYSPKGYTKLGESESLGCSGAAGSGTLELP 344
Db 276 PCAPLAECKSLDDDSAGKSTEDTAESYSPKGYTKLGESESLGCSGAAGSGTLELP 335
QY 345 STLSLYKSGALDEAAAYQSDRYNFPALAGPPPPPPPPHARIKLENPDLGYSAWAAA 404
Db 336 SSLSLYKSGALDEAAAYQSDRYNFPALAGPPPPPPPPHARIKLENPDLGYSAWAAA 395
QY 405 AAQCRYGDLASLHGAAGAGCGSPSAAASSWHTLFTAEEOGLYPCGGGGGGGGGG 464
Db 396 AAQCRYGDLASLHGAAGAGCGSPSAAASSWHTLFTAEEOGLYPCGGGGGGGGGG 442
QY 465 GGGGGGGGGGGGAGAVAPGYTRPPGCLAGQSDFTAPDVPVPGWMSRVYPSPCTVK 524
Db 443 --GGGGGGSSPSDAGVPAPGYTRPPGCLAGQSDFTAPDVPVPGWMSRVYPSPCTVK 500
QY 525 SEMGPWMDSYSGPYGDMRLTARDHVLPIDYFPPOKTCILCDEASGCHYGALTCGSK 584
Db 501 SEMGPWMDSYSGPYGDMRLTARDHVLPIDYFPPOKTCILCDEASGCHYGALTCGSK 560
QY 585 VFFKRAEGKQKYLACARNDCITDKFRKNCPCRLKCYEAGMTLGARKKLKGLNKLQ 644
Db 561 VFFKRAEGKQKYLACARNDCITDKFRKNCPCRLKCYEAGMTLGARKKLKGLNKLQ 620
QY 645 EGEASTTSTPTETTKLTVSHTEGYECOPIFLNVLAEIPGVVCAHDNNOPDSFAAL 704
Db 621 EGENSNAGSPTEPDPSOKMTVSHTEGYECOPIFLNVLAEIPGVVCAHDNNOPDSFAAL 680
QY 705 LSSLNELGERQLVHVVKAKALPFRNLHVDQMAVITYQSWMGLMVFAMGWSRFTNVNSR 764
Db 681 LSSLNELGERQLVHVVKAKALPFRNLHVDQMAVITYQSWMGLMVFAMGWSRFTNVNSR 740
QY 765 MLYFAPDLVFNEMRHKSRMYSOCVNRHLSQFEGWLIQTPQBFCLMKALLLSIIPVDG 824
Db 741 MLYFAPDLVFNEMRHKSRMYSOCVNRHLSQFEGWLIQTPQBFCLMKALLLSIIPVDG 800
QY 825 LKNQKFFDELRLMNYIKELDRILACKRNKPTSCSRFFVQLTKLLDSVQPIARELHQFTEDL 884
Db 801 LKNQKFFDELRLMNYIKELDRILACKRNKPTSCSRFFVQLTKLLDSVQPIARELHQFTEDL 860
QY 885 LKSHMYSVDFPEMMAEIIISVQPKILSGVKPKYIHFHTQ 923
Db 861 LKSHMYSVDFPEMMAEIIISVQPKILSGVKPKYIHFHTQ 899

RESULT 9
ANDR_RABIT
ID ANDR_RABIT STANDARD; PRT; 709 AA.
AC P49699;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
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DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR) (FRAGMENT).
GN AR OR NR3C4.
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN NCBI_TaxID=9986;
RL 11
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Prostate;
RX MEDLINE=96044663; PubMed=7559153;
RA Krongrad A., Wilson J.D., McPhaul M.J.;
RT "Cloning and partial sequence of the rabbit androgen receptor:
RT expression in fetal urogenital tissues.";
RL J. Androl. 16:209-214 (1995).
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U16366; AAC48469.1; -.
CC HSP: P06536; IRGD.
CC InterPro; IPR001103; Androgen_recep.
CC InterPro; IPR000536; Hormone_rec_1lg.
CC InterPro; IPR001628; zf-C4.
CC Pfam; PF02166; Androgen_recep; 1.
CC Pfam; PF00104; hormone_rec; 1.
CC SMART; SM00105; zf-C4; 1.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; ZnF_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC zinc-finger; Steroid-binding.
FT DON_TER 1
FT DONAIN <1 347 MODULATING.
FT DNA_BIND 349 414 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 349 369 C4-TYPE.
FT ZN_FING 385 409 C4-TYPE.
FT DONAIN 480 709 LIGAND-BINDING.
FT DONAIN 3 6 POLY-GLN.
FT DONAIN 182 187 POLY-PRO.
FT DONAIN 201 207 POLY-ALA.
FT DONAIN 254 262 POLY-GLY.
SQ SEQUENCE 709 AA; 77391 MW; 40E7666137E97B6B CRC64;
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Query Match 71.4%; Score 3509.5; DB 1; Length 709;
Best Local Similarity 90.9%; Pred. No. 3.1e-159;
Matches 660; Conservative 16; Mismatches 31; Indels 19; Gaps 3;

QY 198 QQQQAVSEGGSSSGRRAREASGAPTSSKDNLYLGGTSTISDNKELCKAVSMGLGVLEA 257
Db 3 QQQQDAATEGGSSSGRRARRPSGASTSSKDSYLGSTSVISDSAKELCKAVSMGLGVLEA 62

QY 258 HLSPEQLRGDCMYAPILCVPAVRPTCAPLAECKSLDDDSAGKSTEDTAESYSPKGG 317
Db 63 HLSGEGQLRGDCMYAPILGGPPVVRPTCLPLVECKSLDDDDGPKGTETAEYTPKGG 122

QY 318 YTKGLESGSLGCSGSAAGSGGTLEPSTLSLYKSGALDEAAAYQSDRYNFPALAGPP 377
Db 123 YNKGLESLGCSGSGEAGSSGTLLEPSTLSLYKSGTLDEAAAYQSDRYNFPALAG-- 180
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Db	128	-----QPSPACEVTSSMCLFGPELP-----EDPPAADATQRVLSPLMSRSGCKVGD	174
QY	177	SSCSADLKDILSE--ASTWQLI-----QQOOQEEAVSGSSSGRAREASGA	219
Db	175	SGCTAAAHKVLPRGLSPARQLLPASESPHNSGAPVKFSPQAAAVEVEEDGSESEESAG	234
QY	220	P-TSSKDNVILGTSTISDNA-----KELCKAVSYSMGLGVPEALHLSLSPGE	263
Db	235	PLLKGPRAALGAGAGGAAAVPPGAAAGGVALPKEDSRFSAPRVAL-VEODAPMAPGR	293
QY	264	QLRG-----DCMWAPLLGVPPAVRPTPCAPLAECKSLDLDGAGKSTEDTAYSFPGGYT	319
Db	294	SPLATVWDFIHPIL-----PLNHALLAARTQLLEDES-----YDGGAGAAS	337
QY	320	KGLEGSLOCSSG--AAAGSSGTLELP-----STLSLY-----KSGALDE	357
Db	338	AFAPPRSSPCASSTPVAVGDFPDCAYPDAEPKDDAYPLYSDFOPPALKIKEEEGA--E	395
QY	358	AAAYQSRDYY-----NPLALAGPPPPPPPPHAPHARIKLENPLDYSAWAAAAAQ	407
Db	396	ASARSRSYLVAGANPAAPDFPLP---GPPPPPLPP-----RATP	431
QY	408	CRYGDLASLHGAGAAGPGSGPSAAASSWH--TLFTAE-----EGOLYPCGGGGGGG	459
Db	432	SRPGE-----AAVTAAPASASYSSASSSGSTLECLTYKAEGAPPQQGFPAPPCKAPGAS	486
QY	460	GGGGGGGGGGGGGGGAGAVAPYCTTPPOGLAGQESDFTAPDVWYGGMVSR-VPYP	518
Db	487	GCLLPDRGLPSTSASAAAAA-APALY--PALGLNG-----LPOLGYQAAVVKLEGLPQV	537
QY	519	SPTCVKSEMPWMDSYSGPYGDMRLETADRHVLPIDYFP--PQKTCITCGDEASGCHYG	576
Db	538	YPPYL-NYLRPDSEASQP-----QYSESELPQKICLCIGDEASGCHYG	580
QY	577	ALTCGCKVFFKRAEKGKOKYLCASRNDCTIDKFRKNCPCSLRKCYPAGMTLCARLKL	636
Db	581	VLTCGCKVFFKRAEKGQHNYLCCAGENDCTVDKIRKNCPCALRCKCOAGMVLGGRKFK	640
QY	637	KLGNLKLGEEGASSTSP-----FEETQKLTVSHIGYECQPIFLNVLAEIPGVVC	690
Db	641	KFNKRVVRALDAVALPOPLGVNESAQLSQRTFSPGQDIQLIPPLINLMSIEPDVIY	700
QY	691	AGHDNNQDFAALLSLNELGERQLVHVVKAKALPGFRNLHVDDQMAVIOYSWMGLMV	750
Db	701	AGHDNTKPTSSLLTSLNQLGERQLLSVVVKWSKSLPGFRNLHIDQJITLIQYSWMSLMV	760
QY	751	FAMGWRFTVNSRMLYFADPLVFNERYRMHKSRYMSQCYVMRHLSEFGWLQITPQEFCL	810
Db	761	FLGWRSYKHVSGOMLYFADPLILNEORMKSESFYSLCITMWOIPOEFVKLVQSQEFCL	820
QY	811	MKALLFSITPVDGLKNQKPFDELRMNYIKELDRITACKRKNPSTCSRFRYQLTKLDSV	870
Db	821	MKVLLLLNTIPLEGRSQTOFEEMRSSYIRELIKAIGLRQKGVVSSQRFYQLTKLLDNL	880
QY	871	QPIARELHQFTDLLIKSHMVSYDFFPEMMAELISVQPKILSKCKVPIVFH	921
Db	881	HDLVKQLHQLCLNTFIQSRSLVSFEPPEMNSEVIAAQLPKILAGWAKPLLFH	931
RESULT 12			
PRGR_RAT		STANDARD;	
ID	PRGR_RAT	STANDARD;	923 AA.
AC	Q63449;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	PROGESTERONE RECEPTOR (PR).		
GN	PR OR NR3C3		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Placenta;
RX MEDLINE=94130817; Pubmed=8299566;
RA Park-Sarge O.K., Mayo K.E.;
RT "Regulation of the progesterone receptor gene by gonadotropins and
RL cyclic adenosine 3',5'-monophosphate in rat granulosa cells.";
RL Endocrinology 134:709-718(1994).
CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC -----
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CC -----
CC EMBL; L16922; AAA19916.1; ..
CC HSSP; P06401; 1A28.
CC -1- InterPro: IPR000536; Hormone_rec_llg.
CC InterPro: IPR000128; Progect_rcptor.
CC InterPro: IPR001628; zf-C4.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF02161; prog_receptor; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00047; STROIDFINGER.
CC PRINTS; PR00544; PROGESTRONER.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; znF_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Steroid-binding.
CC FT DOMAIN 1 556 MODULATING, PRO-RICH.
CC FT DNA_BIND 557 622 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 557 577 C4-TYPE.
CC FT ZN_FING 593 617 C4-TYPE.
CC FT DOMAIN 671 923 STEROID-BINDING.
CC FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT SEQUENCE 923 AA; 99407 MW; 05384B9656BF22DC CRC64;
CC -----
Query Match 25.1%; Score 1234; DB 1; Length 923;
Best Local Similarity 33.1%; Pred. No. 1.2e-51;
Matches 344; Conservative 129; Mismatches 299; Indels 266; Gaps 39;

QY 15 PKTYRGA-----FQNLFSQSVREIQNGPRHPPEASAAP-----GASLLLLQQQQ 61
DB 19 PSPTHTGSPLLARLDDPQ-----GSHSDASVSWFPISLDRLLFSRSC 65
QY 62 QQQQQQQQQQQQQQQ-----QQQQQQQETSPRQQQQQGGDGSQPAHRRGPTGYL 110
DB 66 QAGELPDEKTONQQLSLDVEGAFSGVEASRRRSRNRAPEKDSRLIDS----- 113
QY 111 VLDEEQQSQPOSALECHPERG-----VPEPGAVAASKGLPQOOLPAPPDE- 157
DB 114 VLDTLAPSGPQSQTSP-ACEAITSWCLGPELPEDPRSPVATKGLSLPMSRPESK 171
QY 158 --DDSA-----PSTLS-----LLGPTF-----PGLSSCSADLK-----ILSPA 190
DB 172 AGDSSGTGAGQKVLPRVSPPRQLLPTSGSAHPWAGVKPSQOAPATVEVEDGGLETEG 231
QY 191 STWOLLOQQQOQEAIVSGSSSGRAEASGAPTSKQNYLGSTTI--SDNAKELCKAVSVM 249
DB 232 SAGFLPLKSRKRALLEGCMSCGGVGTANAPGAAP-----GGVTLVPKEDSRFSAPRVSLQ 284

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[illegible]

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QY 250 GLGV-----EALHLSPEQLRGDCM-----YAPLLGV 277
Db 285 DAPVAPGRSPLATTVVDFTHVPLPLNHALLAARTOLLEGDSYDGGAAAVPFAPPRGS 344
QY 278 PPAVR-PTCAPLAECKGSLDDSGACKSTED-TAIESPFKGGYTKGLESGCSGSA 335
Db 345 PSAPSPVPCGDFPDC-----TYPPEGDPKEDGFVYGEFPPLGLIKEE-----EGTEA 396
QY 336 GSGTLELSTLSLYKSGALDEAAAYQSRDYNNFLALAGAPPPP-PPPHPHARIKLEN 393
Db 397 SRS-----PRPYLL-----AGASAATFDFPL-----PRPPRAPPSRP----- 430
QY 394 PLDYGSAMAAAACQRYGLAS-----LHCAGAAFGSGS-----PSAAASSSWH 438
Db 431 ----GEA-AVAAPSAVSPVSSGSALEICILYKABCAPPTQGSFAPLCKPAPASS----- 481
QY 439 TLFTAEGOLYPCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 498
Db 482 -CLLPRLSLPAAP-----TSSAAPAIY--PPLGLNG--- 509
QY 499 DFTAPDVWVPGGMV-SRVPYPSPTCVKSEMGMWD-----SYSGPYGDMRLTARDH 549
Db 510 ---LQLGQAVLXDSLPOVYP-----PYNLRLPDSEASQSPQYGFDSL----- 552
QY 550 VLPIDYFPPOKTLICGDEASGCHYGALTCGCKVFKAAGKQKYLCAASRNDCTIDK 609
Db 553 -----POKICLICGDEASGCHYGVLTCGCKVFKAAGKQKYLCAASRNDCTIDK 603
QY 610 FRKNCPSRLKCYEAGMTLGARKLKLGNLQOE--EGEA--SSTSPTEET--OKL 663
Db 604 TRKNCPCACRLKCCQAGMVGGRKRFKFNKVRVNRALDGVLPQSAVFPNESOTLGOI 663
QY 664 TVSHIEGYECOPIFLNLVLEAIEPVGVCAGHDNQPFAALLSSNLGELQVHVVKWA 723
Db 664 TFSNQETQLVPLINLILMSIEPDVYAGHNTKPDYSSSLTSLNOLGERQLLSVVKWS 723
QY 724 KALPGFRLHVDQNAVTOYQSWGLMVFAMGWSFTWNSRMLYFAPDLVFNRYMHKSR 783
Db 724 KSLPGFRLHVDQNAVTOYQSWGLMVFAMGWSFTWNSRMLYFAPDLVFNRYMHKSR 783
QY 784 MYSQVRRHLSQEFGLWLOITPQEFELCMKALLFSITPDGLKNQKQFDELWNYKELD 843
Db 784 FYSCLTNWQIPQEFVLOVTHEEFLCKVLLNTLPLEGLRSQSOFEMRSYIRELI 843
QY 844 RIACKKNPTSCRRRYQLTKLDSVQPIARELHOFTFDLLIKSHMVSVDFPEMMAEII 903
Db 844 KAIGLRQGVVPSQRYQLTKLDSLHLVQLHLVCLNTFTIQSRALAVEFPEMMAEVI 903
QY 904 SVQVPKILSGVKPIYFH 921
Db 904 AAQUPKILAGMKPLLFH 921

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RESULT 13

PRGR_CHICK

ID PRGR_CHICK

AC P07812; Q90946;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROGESTERONE RECEPTOR (PR).

GN PCR OR NR3C3.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=88166640; PubMed=3443098;

RA Gronemeyer H., Turcotte B., Quirin-Stricker C., Bocquel M.T.,

RA Meyer M.E., Krozowski Z., Jeltsch J.M., Lerouge T., Garnier J.M.,

RA Chambon P.;

```

RT "The chicken progesterone receptor: sequence, expression and
RL functional analysis."
RN EMBO J. 6:3985-3994(1987).
RP [2]
RX SEQUENCE FROM N.A.
RA MEDLINE=91042592; PubMed=3153474;
RA Conneely O.M., Dobson A.D.W., Tsai M.-J., Beattie W.G., Toft D.O.,
RA Hucky C.S., Zarucki T., Schrader W.T., O'Malley B.W.;
RT "Sequence and expression of a functional chicken progesterone
RL receptor."
RL Mol. Endocrinol. 1:517-525(1987).
RN [3]
RX SEQUENCE OF 128-164 FROM N.A.
RA MEDLINE=86289413; PubMed=2426779;
RA Conneely O.M., Sullivan W.P., Toft D.O., Birnbaumer M., Cook R.G.,
RA Maxwell B.L., Zarucki-Schulz T., Greene G.L., Schrader W.T.,
RA O'Malley B.W.;
RT "Molecular cloning of the chicken progesterone receptor."
RL Science 233:767-770(1986).
RN [4]
RX SEQUENCE OF 417-490 FROM N.A.
RA MEDLINE=86287271; PubMed=2426697;
RA Jeltsch J.M., Krozowski Z., Quirin-Stricker C., Gronemeyer H.,
RA Simpson R.J., Garnier J.M., Krust A., Jacob F., Chambon P.;
RT "Cloning of the chicken progesterone receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 83:5424-5428(1986).
RN [5]
RX DIFFERENCE BETWEEN FORM 1 AND FORM 2.
RA MEDLINE=89340509; PubMed=2760059;
RA Conneely O.M., Kettelberger D.M., Tsai M.-J., Schrader W.T.,
RA O'Malley B.W.;
RT "The chicken progesterone receptor A and B isoforms are products of
RL an alternate translation initiation event."
RL J. Biol. Chem. 264:14062-14064(1989).
RN [6]
RX SEQUENCE FROM N.A. (ALL FORMS).
RA MEDLINE=90154085; PubMed=2303488;
RA Jeltsch J.-M., Turcotte B., Garnier J.-M., Lerouge T., Krozowski Z.,
RA Gronemeyer H., Chambon P.;
RT "Characterization of multiple mRNAs originating from the chicken
RL progesterone receptor gene. Evidence for a specific transcript
RL encoding form A."
RL J. Biol. Chem. 265:3967-3974(1990).
CC -!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
CC THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), A', B AND B';
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: OVIDUCT.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
CC -----
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CC -----
DR EMBL; Y00092; CAA68282.1; -
DR EMBL; M13972; AAA49034.1; -
DR EMBL; M37518; AAA49013.1; -
DR EMBL; M37518; AAA49014.1; -
DR EMBL; M14278; AAA49035.1; -
DR EMBL; M14279; AAA49038.1; -
DR EMBL; M14280; AAA49039.1; -
DR EMBL; M32732; AAA49011.1; -
DR EMBL; M31104; AAA49011.1; JOINED.
DR EMBL; M32726; AAA49011.1; JOINED.

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Job time: 386 sec

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CC PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR3 SUBFAMILY.
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CC -----
DR EMBL; Z66555; CAA91447.1; -.
DR HSSP; P06401; IA28.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR000128; Progester_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF02161; Prog_receptor; 1.
DR Pfam; PF00105; zf-C4; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT NON_TER 1
FT DOMAIN <1 15 MODULATING, PRO-RICH.
FT DNA_BIND 18 83 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 18 38 C4-TYPE.
FT ZN_FING 54 78 C4-TYPE.
FT DOMAIN 128 >377 STEROID-BINDING.
FT NON_TER 377
SQ SEQUENCE 377 AA; 42904 MW; 3141B65587F7493C CRC64;
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Query Match 22.7%; Score 1116; DB 1; Length 377;
Best Local Similarity 55.2%; Pred. No. 1.9e-46;
Matches 201; Conservative 73; Mismatches 84; Indels 6; Gaps 1;

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QY 559 POKTCLICGDEASGCHYGALTCGCKVFEKRAAEKQKYLCAARNDCITDKPRKNCPCSC 618
Db 14 POKICLICGDEASGCHYGVLTCGCKVFEKRAEGQHNYLCAGRNDCIVDKIRKNCPCAC 73
QY 619 RLKRCYEAAGMTGLGKLLKGLKEEGEASSTSP-----TEETOKLTVSHIEGYE 672
Db 74 RLKRCQAGMVLGGRRKFKFNKVRVNRITLDAVALPQVGPINESQALSQRITFPSQDLQ 133
QY 673 COPIFNLVLEAIEPGVVCAGHDNNQPSFAALLSSLNELGERQLVHVYVWAKALPGFRNL 732
Db 134 LIPPLINLLMSIEPDWVYAGHNSKPDTSLSLTSLNQLGERQLLSVVVWKSLSLPGFRNL 193
QY 733 HYDDQMAVTOYSWGLMVFAMGWRSEFTVNSRMLYFADPLVFNEMRHKSRMYSOCVEMR 792
Db 194 HIDDQITLTOYSWMSLMVFGWRSYKHWGQMLYFADPLILNEQRMKSESSFYSLCLTMW 253
QY 793 HLSQEPGLQITPOEFLCMKALLFSIIPDGLKNGKFEDELRMNYIKELDELITACKRKN 852
Db 254 QIPQEVKLQVSQEEFLCMKVLILLNTIPLEGRSQNFEEMRSSYIRELIKATGLRQK 313
QY 853 PTSCSRFYQLTKLDSVQPIARELHQFTDLLIKSHMVSVDFFEMMAEIIISVQVPKILS 912
Db 314 VVPSQRFYQLTKLLDNLHDLYKQLHLYCLNTFIQSRALSVEFFPEMSEVIAAQLPKILA 373
QY 913 GKVK 916
Db 374 GMVK 377
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Search completed: January 3, 2002, 23:13:11

